4. The caffeine showed synergistic effect in this study when used combination with statin against influenza infection.

Conclusions: It indicates that the statin showed anti-influenza virus infectious activity in a murine model. Moreover, it is inexpensive and available, so the statin may can meet the challenge of the next influenza pandemic.

PP-073 Progress in research on the factors of triggering the resistance of influenza viruses to anti-flu drugs such as oseltamivir and the methods of monitoring and prevention of the drug resistance

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Amantadine, rimantadine, zanamivir, oseltamivir are the most common used anti-flu drugs in clinic, the inappropriate use of them could cause resistance and reduce therapy efficacy. The review was focused on the factors of triggering the resistance of influenza viruses to anti-flu drugs such as oseltamivir, the methods of surveillance, monitoring and prevention of the drug resistance. The review would provide theoretical guidance to the reasonable application of anti-flu drugs to reduce the resistance and bring the effect of the drugs to full play.

PP-074 Influenza-related Host Gene Database (IHGDB): an integrated information resource for influenza-related host's genes

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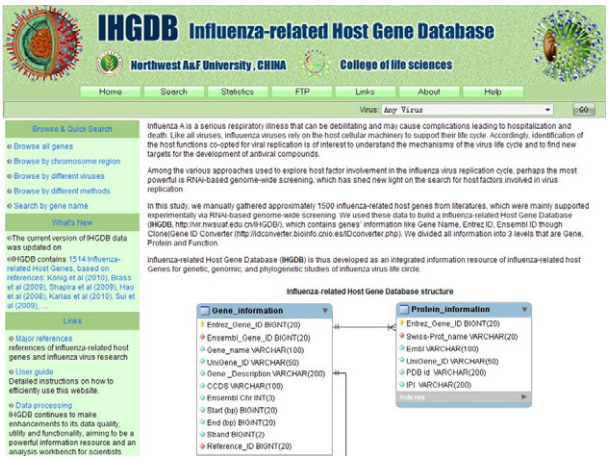
Influenza A is a serious respiratory illness that can be debilitating and may cause complications leading to hospitalization and death. Like all viruses, influenza viruses rely on the host cellular machinery to support their life cycle. Accordingly, in order to understand the mechanisms of the virus life cycle, identification of the host functions co-opted for viral replication is needed and also we can find new targets for the development of antiviral compounds.
In this study, we manually gathered approximately 1500 influenza-related host genes from literatures, which were mainly supported experimentally via RNAi-based genome-wide screening.



We used these data to build a Influenza-related Host Gene Database (IHGDB, http://vir.nwsuaf.edu.cn/IHGDB/), which contains 3 levels information that are gene, protein and function.
Influenza-related Host Gene Database (IHGDB, http://vir.nwsuaf.edu.cn/IHGDB/) is thus developed as an integrated information resource of influenza-related host Genes for genetic, genomic, and phylogenetic studies of influenza virus life circle. It provides a user-friendly interface by which interested genes can easily retrieved by searching engine.

Poster Session – Gastro-intestinal Infections

PP-075 Obstructive jaundice promotes intestinal barrier dysfunction and bacterial translocation: experimental study

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Background: Although clinical and experimental studies have demonstrated a correlation between obstructive jaundice and the development of sepsis, the mechanism has not been fully elucidated.
Aim: to investigate the influence of biliary obstruction on bacterial translocation as a possible source of infection in cases of obstructive jaundice.
Material and Methods: Two groups of 12 Wistar rats were examined: rats subjected to common bile duct (CBD) ligation (group A) and rats subjected to a sham operation (group B). After 7 days blood samples were taken and liver, spleen, and mesenteric lymph nodes (MLN) from the ileocaecal area were removed, divided into small pieces and cultured. Quantitative culture results were determined by the number of colony-forming units (CFU) per ml homogenate. Bacterial translocation was defined as the presence of a positive culture of mesentericlymph nodes, blood, liver and/or spleen. Samples for histopathological examination were taken from the mucosa of the ileum and the colon and evaluated for inflammatory and destructive changes.
Results: There was no evidence of bacterial translocation to MLN, blood, spleen or liver detected in any of the 12 sham-operated control rats. In contrast, bacterial translocation was demonstrated in 8 of the 12 CBD ligated rats ($P < 0.01$). In all 8 cases in which translocation occurred, *Escherichia coli* were cultured from the mesenteric lymph nodes. There were no histological changes in the mucosal samples of the control animals. In the CBD ligated rats hyperemia, vacuolization, reduction of goblet cells, decreased mitotic activity and infiltration by lymphocytes and PMNLs were detected. Cases in which translocation occurred were significantly associated with decreased mitotic activity in the colon ($r = -0.5$, $p < 0.01$) and higher infiltration by PMNLs in the ileum ($r = -0.62$, $p < 0.05$).
Conclusion: Obstructive jaundice in a ratmodel predisposes to bacterial translocation.

PP-076 Impaired Kupffer cell function: a major predisposing factor of septic complications in obstructive jaundice

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Obstructive jaundice is frequently associated with septic complications.
Aim: The aim of this study was to investigate the effect of obstructive jaundice on Kupffer cell functions and its role in septic complications.

Methods: Two groups of Wistar rats were examined: rats subjected to common bile duct ligation (CBDL) and rats subjected to a sham operation. Bacterial clearance, organ distribution and phagocytic function of Kupffer cells were examined.
Results: In this study, clearance of *Escherichia coli* from the peripheral blood in CBDL rats was decreased significantly compared with that in sham-operated rats. A significant decrease in *E. coli* trapped in the liver was observed in CBDL rats compared with sham-operated rats. Phagocytic activity and superoxide production of Kupffer cells isolated from CBDL rats were significantly lower than in sham-operated rats.
Conclusion: The results suggest that susceptibility to infection in obstructive jaundice is due to impaired phagocytic function of Kupffer cells.

PP-078 Genetic characteristics and pathogenicity of hepatitis E virus isolated from patients in eastern China, genotype 4 HEV can result in acute liver failure

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Background and Aims: Hepatitis E is the most important cause of acute viral hepatitis in adults throughout Asia, the Middle East and Africa where the sanitation conditions are usually substandard. The aim of this study was to investigate the genetic characterization of hepatitis E virus (HEV) and its correlation with pathogenicity in patients with or without chronic liver disease and also the phylogenetic relationship between human and swine HEV to assess potential risky factor for sporadic hepatitis E.
Methods: 62 serum samples of patients with acute hepatitis E were collected, including 23 cases coinfected with hepatitis B virus (HBV). The clinical information (age, sex, complication, mortality, markers of liver function) of patients with liver failure were recorded. Anti-HEV detection and partial HEV RNA amplification were performed by enzyme immunoassays (EIA) and reverse transcription-nested polymerase chain reaction (RT-nPCR) method respectively, PCR products were sequenced. The isolated human HEV sequences were analyzed phylogenetically.
Results: 10 of 62 cases suffered from liver failure. The positive rate of HEV RNA in serum were 21.0% (13/62), including 4 patients with liver failure. All 13 isolates shared 82.1%-98.0% nucleotide homology with each other and had identities of 74.7%-81.0%, 75.3%-78.6%, 75.3%-80.0% and 82.1%-96.1% with the corresponding regions of genotypes 1–4 HEV respectively. One human HEV strain (GS-NJ-12) shared 100% nucleotide identity with the swine HEV strain named swIM6–43.
Conclusions: This study provides further evidence supporting the possibility of zoonotic transmission of HEV from swine to human, genotype 4 HEV can result in acute liver failure and acute-on-chronic failure.

PP-079 Abnormal expression of IGF-II in HBV-related liver diseases and influences of activation intervention on prolification of HepG2 cells

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Background: The abnormality of IGF-II expressions involved in the formation and development of HCC. However, their molecular mechanism and expression rule remains not too clear. In the present study, we investigated the levels of IGF-II expression in cancerous, paracancerous, noncancerous tissues, and circulating blood in HCC patients, and the clinicopathological features of IGF-II abnormality, and analyze the effect of specific siRNA-mediated inhibition of IGF-II on apoptosis of human HepG2 cells.
Methods: The levels of circulating IGF-II in patients with liver diseases and 30 healthy individuals were detected by ELISA. IGF-IIsiRNA was used to down-regulate IGF-II expression in human HepG2 cells; RT-PCR and ELISA were used to examine IGF-II expression; Annexin V-FLUOS/PI was used to test cell apoptosis.
Results: The expression of IGF-II in peripheral blood of HCC patients was significantly more than patients with non-liver tumors, acute or chronic hepatitis, liver cirrhosis, and normal subjects ($P = 0.000$). The overexpression of IGF-II in the cancerous group was associated with HBV infection. At 72 h after IGF-IIsiRNA transfection, IGF-II expression in the 150 nM group in the HepG2 cells reduced 63% at mRNA and 44.5% at protein levels. The down-regulation of IGF-II expression was depended on the dose of IGF-IIsiRNA and the action time after specific siRNA transfection. Interestingly, the apoptosis index of the HepG2 cells increased with IGF-II inhibition, and the down-regulation of IGF-II sensitized HepG2 cells to adriamycin.
Conclusion: The abnormal activation of hepatic IGF-II is closely associated with the occurrence and development of HCC, and IGF-II inhibition mediated by specific siRNA promotes HepG2 cells apoptosis. Therefore IGF-II is a potential target for HCC gene therapy.

PP-080 Investigation on MMP-9 concentration in sera of people infected by *Helicobacter pylori*

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Objectives: Helicobacter Pylori (HP), as a gram negative bacterium colonizing in the gastric mucosa, induces gastrodeudenal complications varying from mild gastritis to gastric malignancies. mmp-9, an enzyme with protease activity, plays key role in cancer induction and metathesis. Regarding to high incidence of gastric cancer in Ardabil province, the present study was conducted with the following major question whether the increase of serum level of mmp-9 can be seen before induction of cancer by H.P.
Methods: Serum and stool specimens together were obtained from 200 apparently healthy individuals. Samples were stored at –70ºC until ELISA experiments. ELISA kits were used to assess H. Pylori Ag in stools and serum concentration of mmp-9.
Results: Obtained results showed increase of serum level of mmp-9 in H.P infected person in comparison to healthy ones.
Discussion: Albeit our results show increase in serum level of mmp-9 in infected persons but this is not significant. Previous studies showed significant increase in mmp-9 concentration in biopsy samples prepared from H.P. infected persons. This controversy may arise from differences in studied population, variety of H.P., the manner of sampling and detection of H.P. infection. We suggest making a similar investigation with special regards to these factors.